

SEQUENCE LISTING

<110> Meyers, Rachel
Hunter, John Joseph

<120> 62112, A NOVEL HUMAN DEHYDROGENASE AND
USES THEREOF

<130> MNI-187

<150> 60/229,831

<151> 2000-08-31

<160> 3

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2452

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (67)...(1932)

<400> 1

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ggcagc atg agc ggc tgc ggg ctc ttc ctg cgc acc acg gct gcg gct 108
      Met Ser Gly Cys Gly Leu Phe Leu Arg Thr Thr Ala Ala Ala
        1             5             10

cgt gcc tgc cgg ggt ctg gtg gtc tct acc gcg aac cgg cgg cta ctg 156
Arg Ala Cys Arg Gly Leu Val Val Ser Thr Ala Asn Arg Arg Leu Leu
  15             20             25             30

cgc acc agc ccg cct gta cga gct ttc gcc aaa gag ctt ttc cta ggc 204
Arg Thr Ser Pro Pro Val Arg Ala Phe Ala Lys Glu Leu Phe Leu Gly
              35             40             45

aaa atc aag aag aaa gaa gtt ttc cca ttt cca gaa gtt agc caa gat 252
Lys Ile Lys Lys Lys Glu Val Phe Pro Phe Pro Glu Val Ser Gln Asp
      50             55             60

gaa ctt aat gaa atc aat cag ttc ttg gga ccc gtg gaa aaa ttc ttc 300
Glu Leu Asn Glu Ile Asn Gln Phe Leu Gly Pro Val Glu Lys Phe Phe
      65             70             75

act gaa gag gtg gac tcc cga aaa att gac cag gaa ggg aaa atc cca 348
Thr Glu Glu Val Asp Ser Arg Lys Ile Asp Gln Glu Gly Lys Ile Pro
      80             85             90

gat gaa act ttg gag aaa ttg aag agc cta ggg ctt ttt ggg ctg caa 396
Asp Glu Thr Leu Glu Lys Leu Lys Ser Leu Gly Leu Phe Gly Leu Gln
      95             100             105             110

gtc cca gaa gaa tat ggt ggc ctg ggc ttc tcc aac acc atg tac tca 444
Val Pro Glu Glu Tyr Gly Gly Leu Gly Phe Ser Asn Thr Met Tyr Ser
      115             120             125

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09945336-083101

[illegible]

Leu	Asp	Gln	Pro 370	Gly	Phe	Pro	Asp	Cys 375	Ser	Ile	Glu	Ala	Ala 380	Met	Val	
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cag Gln	atc Ile 400	ctc Leu	ggg Gly	ggc Gly	ttg Leu	ggc Gly 405	tac Tyr	aca Thr	agg Arg	gac Asp	tat Tyr 410	ccg Pro	tac Tyr	gag Glu	cgc Arg	1308
ata Ile 415	ctg Leu	cgt Arg	gac Asp	acc Thr	cgc Arg 420	atc Ile	ctc Leu	ctc Leu	atc Ile	ttc Phe 425	gag Glu	gga Gly	acc Thr	aat Asn	gag Glu 430	1356
att Ile	ctc Leu	cgg Arg	atg Met	tac Tyr 435	atc Ile	gcc Ala	ctg Leu	acg Thr	ggg Gly 440	ctg Leu	cag Gln	cat His	gcc Ala	ggc Gly 445	cgc Arg	1404
atc Ile	ctg Leu	act Thr	acc Thr 450	agg Arg	atc Ile	cat His	gag Glu	ctt Leu 455	aaa Lys	cag Gln	gcc Ala	aaa Lys	gtg Val 460	agc Ser	aca Thr	1452
gtc Val	atg Met	gat Asp 465	acc Thr	gtt Val	ggc Gly	cgg Arg	agg Arg 470	ctt Leu	cgg Arg	gac Asp	tcc Ser	ctg Leu 475	ggc Gly	cga Arg	act Thr	1500
gtg Val	gac Asp 480	ctg Leu	ggg Gly	ctg Leu	aca Thr	ggc Gly 485	aac Asn	cat His	gga Gly	gtt Val	gtg Val 490	cac His	ccc Pro	agt Ser	ctt Leu	1548
gcg Ala 495	gac Asp	agt Ser	gcc Ala	aac Asn	aag Lys 500	ttt Phe	gag Glu	gag Glu	aac Asn	acc Thr 505	tac Tyr	tgc Cys	ttc Phe	ggc Gly	cgg Arg 510	1596
acc Thr	gtg Val	gag Glu	aca Thr	ctg Leu 515	ctg Leu	ctc Leu	cgc Arg	ttt Phe 520	ggc Gly	aag Lys	acc Thr	atc Ile	atg Met	gag Glu 525	gag Glu	1644
cag Gln	ctg Leu	gta Val	ctg Leu 530	aag Lys	cgg Arg	gtg Val	gcc Ala 535	aac Asn	atc Ile	ctc Leu	atc Ile	aac Asn	ctg Leu 540	tat Tyr	ggc Gly	1692
atg Met	acg Thr	gcc Ala 545	gtg Val	ctg Leu	tcg Ser	cgg Arg	gcc Ala 550	agc Ser	cgc Arg	tcc Ser	atc Ile	cgc Arg 555	att Ile	ggg Gly	ctc Leu	1740
cgc Arg	aac Asn 560	cac His	gac Asp	cac His	gag Glu	gtt Val 565	ctc Leu	ttg Leu	gcc Ala	aac Asn	acc Thr 570	ttc Phe	tgc Cys	gtg Val	gaa Glu	1788
gct Ala 575	tac Tyr	ttg Leu	cag Gln	aat Asn	ctc Leu 580	ttc Phe	agc Ser	ctc Leu	tct Ser	cag Gln	ctg Leu	gac Asp	aag Lys	tat Tyr	gct Ala 590	1836
cca Pro	gaa Glu	aac Asn	cta Leu	gat Asp 595	gag Glu	cag Gln	att Ile	aag Lys	aaa Lys 600	gtg Val	tcc Ser	cag Gln	cag Gln	atc Ile 605	ctt Leu	1884
gag Glu	aag Lys	cga Arg	gcc Ala	tat Tyr	atc Ile	tgt Cys	gcc Ala	cac His	cct Pro	ctg Leu	gac Asp	agg Arg	aca Thr	tgc Cys	tga *	1932

610

615

620

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ggcagggggac agtgtcccct gctaccgccc gccccctaccc atggcccgtt gctggatgac 1992
tggtactctt ttttcagaag gtgttgggat taccacaggt taagcctttt gttccccgtc 2052
tgcacctgaa ggggtgtcgc ctggcctggg agagcctctt ccaggttttg acctgcaggc 2112
agtgtctctt aacaggacca tcacagcttc tgaactgagc cggagagaga gaatggaatt 2172
gctgacctct ggaactggcg ggtattcttg tcattgagga gacaccatag tggaaactgg 2232
ggcttatgct gctgcctcca ggggtgtgagg tgggtgggga cctgtgtcag gtgtggatag 2292
ccatttctgc tcaaccacac attctctaag aaacagcttg aaagctctgt ctgggtcatt 2352
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<210> 2

<211> 621

<212> PRT

<213> Homo sapiens

<400> 2

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Cys Arg Gly Leu Val Val Ser Thr Ala Asn Arg Arg Leu Leu Arg Thr
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Ser Pro Pro Val Arg Ala Phe Ala Lys Glu Leu Phe Leu Gly Lys Ile
 35          40          45
Lys Lys Lys Glu Val Phe Pro Phe Pro Glu Val Ser Gln Asp Glu Leu
 50          55          60
Asn Glu Ile Asn Gln Phe Leu Gly Pro Val Glu Lys Phe Phe Thr Glu
 65          70          75          80
Glu Val Asp Ser Arg Lys Ile Asp Gln Glu Gly Lys Ile Pro Asp Glu
 85          90          95
Thr Leu Glu Lys Leu Lys Ser Leu Gly Leu Phe Gly Leu Gln Val Pro
100          105          110
Glu Glu Tyr Gly Gly Leu Gly Phe Ser Asn Thr Met Tyr Ser Arg Leu
115          120          125
Gly Glu Ile Ile Ser Met Asp Gly Ser Ile Thr Val Thr Leu Ala Ala
130          135          140
His Gln Ala Ile Gly Leu Lys Gly Ile Ile Leu Ala Gly Thr Glu Glu
145          150          155          160
Gln Lys Ala Lys Tyr Leu Pro Lys Leu Ala Ser Gly Glu His Ile Ala
165          170          175
Ala Phe Cys Leu Thr Glu Pro Ala Ser Gly Ser Asp Ala Ala Ser Ile
180          185          190
Arg Ser Arg Ala Thr Leu Ser Glu Asp Lys Lys His Tyr Ile Leu Asn
195          200          205
Gly Ser Lys Val Trp Ile Thr Asn Gly Gly Leu Ala Asn Ile Phe Thr
210          215          220
Val Phe Ala Lys Thr Glu Val Val Asp Ser Asp Gly Ser Val Lys Asp
225          230          235          240
Lys Ile Thr Ala Phe Ile Val Glu Arg Asp Phe Gly Gly Val Thr Asn
245          250          255
Gly Lys Pro Glu Asp Lys Leu Gly Ile Arg Gly Ser Asn Thr Cys Glu
260          265          270
Val His Phe Glu Asn Thr Lys Ile Pro Val Glu Asn Ile Leu Gly Glu
275          280          285
Val Gly Asp Gly Phe Lys Val Ala Met Asn Ile Leu Asn Ser Gly Arg
290          295          300
Phe Ser Met Gly Ser Val Val Ala Gly Leu Leu Lys Arg Leu Ile Glu
305          310          315          320
Met Thr Ala Glu Tyr Ala Cys Thr Arg Lys Gln Phe Asn Lys Arg Leu
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[illegible]

<211> 1863

<213> Homo sapiens

<221> CDS

<222> (1) ... (1863)

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1 5 10 15

tgc	cgg	ggt	ctg	gtg	gtc	tct	acc	gcg	aac	cgg	cgg	cta	ctg	cgc	acc	96
Cys	Arg	Gly	Leu	Val	Val	Ser	Thr	Ala	Asn	Arg	Arg	Leu	Leu	Arg	Thr	
			20					25					30			

agc ccg cct gta cga gct ttc gcc aaa gag ctt ttc cta ggc aaa atc 144
Ser Pro Pro Val Arg Ala Phe Ala Lys Glu Leu Phe Leu Gly Lys Ile
35 40 45

aag aag aaa gaa gtt ttc cca ttt cca gaa gtt agc caa gat gaa ctt 192
Lys Lys Lys Glu Val Phe Pro Phe Pro Glu Val Ser Gln Asp Glu Leu

[illegible]

gcc	gtg	ctg	tcg	cgg	gcc	agc	cgc	tcc	atc	cgc	att	ggg	ctc	cgc	aac	1680
Ala	Val	Leu	Ser	Arg	Ala	Ser	Arg	Ser	Ile	Arg	Ile	Gly	Leu	Arg	Asn	
545					550					555					560	
cac	gac	cac	gag	gtt	ctc	ttg	gcc	aac	acc	ttc	tgc	gtg	gaa	gct	tac	1728
His	Asp	His	Glu	Val	Leu	Leu	Ala	Asn	Thr	Phe	Cys	Val	Glu	Ala	Tyr	
			565						570						575	
ttg	cag	aat	ctc	ttc	agc	ctc	tct	cag	ctg	gac	aag	tat	gct	cca	gaa	1776
Leu	Gln	Asn	Leu	Phe	Ser	Leu	Ser	Gln	Leu	Asp	Lys	Tyr	Ala	Pro	Glu	
			580					585					590			
aac	cta	gat	gag	cag	att	aag	aaa	gtg	tcc	cag	cag	atc	ctt	gag	aag	1824
Asn	Leu	Asp	Glu	Gln	Ile	Lys	Lys	Val	Ser	Gln	Gln	Ile	Leu	Glu	Lys	
		595					600					605				
cga	gcc	tat	atc	tgt	gcc	cac	cct	ctg	gac	agg	aca	tgc				1863
Arg	Ala	Tyr	Ile	Cys	Ala	His	Pro	Leu	Asp	Arg	Thr	Cys				
	610					615					620					

09945326 033404